



COPY OF PATENT  
ORIGINAL FILE

#16

# SEQUENCE LISTING

<110> Civelli Olivier  
Bunzow, James R.  
Grandy, David K.  
Machida, Curtis A.

<120> Dopamine Receptors and Genes

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Xaa (78) residue can be Phe, Ser, Tyr, Cys, Leu, Pro, His, Arg, Ile, Thr, Asn, Val, Ala, Asp or Gly

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cag ctg act ctc ccc gac ccg tcc cac cat ggt ctc cac agc act ccc 97
Gln Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro
      20           25           30

gac agc ccc gcc aaa cca gag aag aat ggg cat gcc aaa agg acc acc 145
Asp Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr
      35           40           45

cca agg att gcc aag atc ttt gag atc cag acc atg ccc aat ggc aaa 193
Pro Arg Ile Ala Lys Ile Phe Glu Ile Gln Thr Met Pro Asn Gly Lys
      50           55           60

acc cgg acc tcc ctc aag acc atg agc cgt agg aag ntc nnc cag cag 241
Thr Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Xaa Xaa Gln Gln
      65           70           75           80

aag gag aag aaa gcc act cag atg ctc gcc atn gtt ctc ggc gtg ttc 289
Lys Glu Lys Lys Ala Thr Gln Met Leu Ala Xaa Val Leu Gly Val Phe
      85           90           95

atc atc tgc tgg ctg ccc ttc ttc atc aca cac atc ctg aac ata cac 337
Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His
      100          105          110

tgt gac tgc aac atc ccg cct gtc ctg tac agc gcc ttc acg tgg ctg 385
Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu
      115          120          125

ggc tat gtc aac agc gcc gtg aac ccc atc atc tac acc acc ttc aac 433
Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn
      130          135          140

att gag ttc cgc aag gcc ttc ctg aag atc ctc cac tgc tgactctgct 482
Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys
      145          150          155

gcctgccgca cagcagcctg cttccacct ccctgccag tgccggccag cctcaccctt 542

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gcgaaccgtg agcaggaagg cctgggtgga tcggcctcct cttctagccc cg

594

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<213> Homo sapiens

<220>  
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<223> Xaa (77) residue can be Phe, Leu, Ile, or Val  
Xaa (78) residue can be Phe, Ser, Tyr, Cys, Leu, Pro, His, Arg,  
Ile, Thr, Asn, Val, Ala, Asp or Gly

<220>  
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<222> (91)  
<223> Xaa (91) residue can be Ile or Met

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Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His  
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Gln Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro  
20 25 30  
Asp Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Arg Thr Thr  
35 40 45  
Pro Arg Ile Ala Lys Ile Phe Glu Ile Gln Thr Met Pro Asn Gly Lys  
50 55 60  
Thr Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Xaa Xaa Gln Gln  
65 70 75 80  
Lys Glu Lys Lys Ala Thr Gln Met Leu Ala Xaa Val Leu Gly Val Phe  
85 90 95  
Ile Ile Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His  
100 105 110  
Cys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu  
115 120 125  
Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn  
130 135 140  
Ile Glu Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys  
145 150 155

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<220>

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<222> (34)..(1362)

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                               1           5

tgg tat gat gat gat ctg gag agg cag aac tgg agc cgg ccc ttc aac 102
Trp Tyr Asp Asp Asp Leu Glu Arg Gln Asn Trp Ser Arg Pro Phe Asn
          10           15           20

ggg tca gac ggg aag gcg gac aga ccc cac tac aac tac tat gcc aca 150
Gly Ser Asp Gly Lys Ala Asp Arg Pro His Tyr Asn Tyr Tyr Ala Thr
          25           30           35

ctg ctc acc ctg ctc atc gct gtc atc gtc ttc ggc aac gtg ctg gtg 198
Leu Leu Thr Leu Leu Ile Ala Val Ile Val Phe Gly Asn Val Leu Val
          40           45           50           55

tgc atg gct gtg tcc cgc gag aag gcg ctg cag acc acc acc aac tac 246
Cys Met Ala Val Ser Arg Glu Lys Ala Leu Gln Thr Thr Thr Asn Tyr
          60           65           70

ctg atc gtc agc ctc gca gtg gcc gac ctc ctc gtc gcc aca ctg gtc 294
Leu Ile Val Ser Leu Ala Val Ala Asp Leu Leu Val Ala Thr Leu Val
          75           80           85

atg ccc tgg gtt gtc tac ctg gag gtg gta ggt gag tgg aaa ttc agc 342
Met Pro Trp Val Val Tyr Leu Glu Val Val Gly Glu Trp Lys Phe Ser
          90           95           100

agg att cac tgt gac atc ttc gtc act ctg gac gtc atg atg tgc acg 390
Arg Ile His Cys Asp Ile Phe Val Thr Leu Asp Val Met Met Cys Thr
          105           110           115

gcg agc atc ctg aac ttg tgt gcc atc agc atc gac agg tac aca gct 438
Ala Ser Ile Leu Asn Leu Cys Ala Ile Ser Ile Asp Arg Tyr Thr Ala
          120           125           130           135

gtg gcc atg ccc atg ctg tac aat acg cgc tac agc tcc aag cgc cgg 486
Val Ala Met Pro Met Leu Tyr Asn Thr Arg Tyr Ser Ser Lys Arg Arg
          140           145           150

gtc acc gtc atg atc tcc atc gtc tgg gtc ctg tcc ttc acc atc tcc 534
Val Thr Val Met Ile Ser Ile Val Trp Val Leu Ser Phe Thr Ile Ser
          155           160           165

tgc cca ctc ctc ttc gga ctc aat aac gca gac cag aac gag tgc atc 582
Cys Pro Leu Leu Phe Gly Leu Asn Asn Ala Asp Gln Asn Glu Cys Ile
          170           175           180

att gcc aac ccg gcc ttc gtg gtc tac tcc tcc atc gtc tcc ttc tac 630
Ile Ala Asn Pro Ala Phe Val Val Tyr Ser Ser Ile Val Ser Phe Tyr
          185           190           195
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gtg ccc ttc att gtc acc ctg ctg gtc tac atc aag atc tac att gtc	678
Val Pro Phe Ile Val Thr Leu Leu Val Tyr Ile Lys Ile Tyr Ile Val	
200 205 210 215	
ctc cgc aga cgc cgc aag cga gtc aac acc aaa cgc agc agc cga gct	726
Leu Arg Arg Arg Arg Lys Arg Val Asn Thr Lys Arg Ser Ser Arg Ala	
220 225 230	
ttc agg gcc cac ctg agg gct cca cta aag ggc aac tgt act cac ccc	774
Phe Arg Ala His Leu Arg Ala Pro Leu Lys Gly Asn Cys Thr His Pro	
235 240 245	
gag gac atg aaa ctc tgc acc gtt atc atg aag tct aat ggg agt ttc	822
Glu Asp Met Lys Leu Cys Thr Val Ile Met Lys Ser Asn Gly Ser Phe	
250 255 260	
cca gtg aac agg cgg aga gtg gag gct gcc cgg cga gcc cag gag ctg	870
Pro Val Asn Arg Arg Arg Val Glu Ala Ala Arg Arg Ala Gln Glu Leu	
265 270 275	
gag atg gag atg ctc tcc agc acc agc cca ccc gag agg acc cgg tac	918
Glu Met Glu Met Leu Ser Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr	
280 285 290 295	
agc ccc atc cca ccc agc cac cac cag ctg act ctc ccc gac ccg tcc	966
Ser Pro Ile Pro Pro Ser His His Gln Leu Thr Leu Pro Asp Pro Ser	
300 305 310	
cac cat ggt ctc cac agc act ccc gac agc ccc gcc aaa cca gag aag	1014
His His Gly Leu His Ser Thr Pro Asp Ser Pro Ala Lys Pro Glu Lys	
315 320 325	
aat ggg cat gcc aaa gac cac ccc aag att gcc aag atc ttt gag atc	1062
Asn Gly His Ala Lys Asp His Pro Lys Ile Ala Lys Ile Phe Glu Ile	
330 335 340	
cag acc atg ccc aat ggc aaa acc cgg acc tcc ctc aag acc atg agc	1110
Gln Thr Met Pro Asn Gly Lys Thr Arg Thr Ser Leu Lys Thr Met Ser	
345 350 355	
cgt agg aag ctc tcc cag cag aag gag aag aaa gcc act cag atg ctc	1158
Arg Arg Lys Leu Ser Gln Gln Lys Glu Lys Lys Ala Thr Gln Met Leu	
360 365 370 375	
gcc att gtt ctc ggc gtg ttc atc atc tgc tgg ctg ccc ttc ttc atc	1206
Ala Ile Val Leu Gly Val Phe Ile Ile Cys Trp Leu Pro Phe Phe Ile	
380 385 390	
aca cac atc ctg aac ata cac tgt gac tgc aac atc ccg cct gtc ctg	1254
Thr His Ile Leu Asn Ile His Cys Asp Cys Asn Ile Pro Pro Val Leu	
395 400 405	
tac agc gcc ttc acg tgg ctg ggc tat gtc aac agc gcc gtg aac ccc	1302
Tyr Ser Ala Phe Thr Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro	
410 415 420	

atc atc tac acc acc ttc aac att gag ttc cgc aag gcc ttc ctg aag 1350  
 Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala Phe Leu Lys  
 425 430 435

atc ctc cac tgc tgactctgct gcctgcccgc acagcagcct gcttcccacc 1402  
 Ile Leu His Cys  
 440

tccctgccca ggccggccag cctcaccctt gcgaaccgtg agcaggaagg cctgggtgga 1462  
 tcggcctcct cttcttagcc ccggcaggcc ctgcagtgtt cgcttggtc catgctcctc 1522  
 actgcccgc caccctcact ctgccagggc agtgctagtg agctgggcat ggtaccagcc 1582  
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 caggcgggtg ggagagatgg acagttcaca ccctgcaagg cccacaggag gcaagcaagc 1822  
 tctcttgccg aggagccagg caacttcagt cctgggagac ccatgtaaat accagactgc 1882  
 aggttggacc ccaaggattc ccaagccaaa aaccttagct ccctcccgc cccgatgtg 1942  
 gacctctact ttccaggcta gtccggaccc acctacccc gttacagctc cccaagtgg 2002  
 ttccacatgc tctgagaaga ggagccctca tcttgaagg cccaggagg tctatggga 2062  
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 tccactgcct ctgccttaga ggagcccacg gctaagaggc tgctgaaaac catctggcct 2362  
 ggcttgccc tgccctgagg aaggagggca agctgcagct tgggagagcc cctggggcct 2422  
 agactctgta acatcactat ccgatgcacc aaactaataa aactttgacg agtcaccttc 2482

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 <212> PRT  
 <213> Homo sapiens

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 Asn Trp Ser Arg Pro Phe Asn Gly Ser Asp Gly Lys Ala Asp Arg Pro  
 20 25 30



His Tyr Asn Tyr Tyr Ala Thr Leu Leu Thr Leu Leu Ile Ala Val Ile  
 35 40 45  
 Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala  
 50 55 60  
 Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp  
 65 70 75 80  
 Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val  
 85 90 95  
 Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr  
 100 105 110  
 Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile  
 115 120 125  
 Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr  
 130 135 140  
 Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ser Ile Val Trp  
 145 150 155 160  
 Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn  
 165 170 175  
 Ala Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr  
 180 185 190  
 Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val  
 195 200 205  
 Tyr Ile Lys Ile Tyr Ile Val Leu Arg Arg Arg Arg Lys Arg Val Asn  
 210 215 220  
 Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala His Leu Arg Ala Pro Leu  
 225 230 235 240  
 Lys Gly Asn Cys Thr His Pro Glu Asp Met Lys Leu Cys Thr Val Ile  
 245 250 255  
 Met Lys Ser Asn Gly Ser Phe Pro Val Asn Arg Arg Arg Val Glu Ala  
 260 265 270  
 Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser Ser Thr Ser  
 275 280 285  
 Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser His His Gln  
 290 295 300  
 Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser Thr Pro Asp  
 305 310 315 320  
 Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Asp His Pro Lys  
 325 330 335

Ile Ala Lys Ile Phe Glu Ile Gln Thr Met Pro Asn Gly Lys Thr Arg  
340 345 350

Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser Gln Gln Lys Glu  
355 360 365

Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Gly Val Phe Ile Ile  
370 375 380

Cys Trp Leu Pro Phe Phe Ile Thr His Ile Leu Asn Ile His Cys Asp  
385 390 395 400

Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr Trp Leu Gly Tyr  
405 410 415

Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu  
420 425 430

Phe Arg Lys Ala Phe Leu Lys Ile Leu His Cys  
435 440

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<212> DNA  
<213> Rattus norvegicus

<220>  
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<222> (1)..(1245)

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aac tgg agc cgg ccc ttc aat ggg tca gaa ggg aag gca gac agg ccc 96  
Asn Trp Ser Arg Pro Phe Asn Gly Ser Glu Gly Lys Ala Asp Arg Pro  
20 25 30

cac tac aac tac tat gcc atg ctg ctc acc ctc ctc atc ttt atc atc 144  
His Tyr Asn Tyr Tyr Ala Met Leu Leu Thr Leu Leu Ile Phe Ile Ile  
35 40 45

gtc ttt ggc aat gtg ctg gtg tgc atg gct gta tcc cga gag aag gct 192  
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala  
50 55 60

ttg cag acc acc acc aac tac ttg ata gtc agc ctt gct gtg gct gat 240  
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp  
65 70 75 80

ctt ctg gtg gcc aca ctg gta atg ccg tgg gtt gtc tac ctg gag gtg 288  
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val  
85 90 95

gtg ggt gag tgg aaa ttc agc agg att cac tgt gac atc ttt gtc act 336

Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr	
100 105 110	
ctg gat gtc atg atg tgc aca gca agc atc ctg aac ctg tgt gcc atc	384
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile	
115 120 125	
agc att gac agg tac aca gct gtg gca atg ccc atg ctg tat aac aca	432
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr	
130 135 140	
cgc tac agc tcc aag cgc cga gtt act gtc atg att gcc att gtc tgg	480
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ala Ile Val Trp	
145 150 155 160	
gtc ctg tcc ttc acc atc tcc tgc cca ctg ctc ttc gga ctc aac aat	528
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn	
165 170 175	
aca gac cag aat gag tgt atc att gcc aac cct gcc ttt gtg gtc tac	576
Thr Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr	
180 185 190	
tcc tcc att gtc tca ttc tac gtg ccc ttc atc gtc act ctg ctg gtc	624
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val	
195 200 205	
tat atc aaa atc tac atc gtc ctc cgg aag cgc cgg aag cgg gtc aac	672
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn	
210 215 220	
acc aag cgc agc agt cga gct ttc aga gcc aac ctg aag aca cca ctc	720
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu	
225 230 235 240	
aag gat gct gcc cgc cga gct cag gag ctg gaa atg gag atg ctg tca	768
Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser	
245 250 255	
agc acc agc ccc cca gag agg acc cgg tat agc ccc atc cct ccc agt	816
Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser	
260 265 270	
cac cac cag ctc act ctc cct gat cca tcc cac cac ggc cta cat agc	864
His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser	
275 280 285	
aac cct gac agt cct gcc aaa cca gag aag aat ggg cac gcc aag att	912
Asn Pro Asp Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Ile	
290 295 300	
gtc aat ccc agg att gcc aag ttc ttt gag atc cag acc atg ccc aat	960
Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile Gln Thr Met Pro Asn	
305 310 315 320	
ggc aaa acc cgg acc tcc ctt aag acg atg agc cgc aga aag ctc tcc	1008
Gly Lys Thr Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser	

	325	330	335	
cag cag aag gag aag aaa gcc act cag atg ctt gcc att gtt ctc gcc				1056
Gln Gln Lys Glu Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Ala				
	340	345	350	
gtc aac ccc atc atc tac acc acc ttc aac atc gag ttc cgc aag gcc				1104
Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala				
	355	360	365	
ttc atg aag gat tgc aac atc cca cca gtc ctc tac agc gcc ttc aca				1152
Phe Met Lys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr				
	370	375	380	
tgg ctg ggc tat gtc aac agt gcc gtc aac ccc atc atc tac acc acc				1200
Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr				
	385	390	395	400
ttc aac atc gag ttc cgc aag gcc ttc atg aag atc ttg cac tgc tga				1248
Phe Asn Ile Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys				
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His Tyr Asn Tyr Tyr Ala Met Leu Thr Leu Leu Ile Phe Ile Ile				
35 40 45				
Val Phe Gly Asn Val Leu Val Cys Met Ala Val Ser Arg Glu Lys Ala				
50 55 60				
Leu Gln Thr Thr Thr Asn Tyr Leu Ile Val Ser Leu Ala Val Ala Asp				
65 70 75 80				
Leu Leu Val Ala Thr Leu Val Met Pro Trp Val Val Tyr Leu Glu Val				
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Val Gly Glu Trp Lys Phe Ser Arg Ile His Cys Asp Ile Phe Val Thr				
100 105 110				
Leu Asp Val Met Met Cys Thr Ala Ser Ile Leu Asn Leu Cys Ala Ile				
115 120 125				
Ser Ile Asp Arg Tyr Thr Ala Val Ala Met Pro Met Leu Tyr Asn Thr				
130 135 140				
Arg Tyr Ser Ser Lys Arg Arg Val Thr Val Met Ile Ala Ile Val Trp				

145		150		155		160
Val Leu Ser Phe Thr Ile Ser Cys Pro Leu Leu Phe Gly Leu Asn Asn						
		165		170		175
Thr Asp Gln Asn Glu Cys Ile Ile Ala Asn Pro Ala Phe Val Val Tyr						
		180		185		190
Ser Ser Ile Val Ser Phe Tyr Val Pro Phe Ile Val Thr Leu Leu Val						
		195		200		205
Tyr Ile Lys Ile Tyr Ile Val Leu Arg Lys Arg Arg Lys Arg Val Asn						
		210		215		220
Thr Lys Arg Ser Ser Arg Ala Phe Arg Ala Asn Leu Lys Thr Pro Leu						
		225		230		235
Lys Asp Ala Ala Arg Arg Ala Gln Glu Leu Glu Met Glu Met Leu Ser						
		245		250		255
Ser Thr Ser Pro Pro Glu Arg Thr Arg Tyr Ser Pro Ile Pro Pro Ser						
		260		265		270
His His Gln Leu Thr Leu Pro Asp Pro Ser His His Gly Leu His Ser						
		275		280		285
Asn Pro Asp Ser Pro Ala Lys Pro Glu Lys Asn Gly His Ala Lys Ile						
		290		295		300
Val Asn Pro Arg Ile Ala Lys Phe Phe Glu Ile Gln Thr Met Pro Asn						
		305		310		315
Gly Lys Thr Arg Thr Ser Leu Lys Thr Met Ser Arg Arg Lys Leu Ser						
		325		330		335
Gln Gln Lys Glu Lys Lys Ala Thr Gln Met Leu Ala Ile Val Leu Ala						
		340		345		350
Val Asn Pro Ile Ile Tyr Thr Thr Phe Asn Ile Glu Phe Arg Lys Ala						
		355		360		365
Phe Met Lys Asp Cys Asn Ile Pro Pro Val Leu Tyr Ser Ala Phe Thr						
		370		375		380
Trp Leu Gly Tyr Val Asn Ser Ala Val Asn Pro Ile Ile Tyr Thr Thr						
		385		390		395
Phe Asn Ile Glu Phe Arg Lys Ala Phe Met Lys Ile Leu His Cys						
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tccccaggtg g 11

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acaggtgagc c 11

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gcaggtacat t 11

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